



SEQUENCE ALIGNMENTS 1-3



SEQUENCE ALIGNMENT 1

		1	50
ADA89581	(1)	MTKHYLNSKYQSEQRSSAMKKITMG TASII LGSLVYIGADSQQVNAATEA	
SEQ1	(1)	-----	
		51	100
ADA89581	(51)	TNATNNQSTQVSOATSQPINFQVQKDGSSSEKSHMDDYMQHPGKVIKQNNK	
SEQ1	(1)	-----MGTQVSOATSQPINFQVQKDGSSSEKSHMDDYMQHPGKVIKQNNK	
		101	150
ADA89581	(101)	YYFQTVLNNASFWKEYKFYNANNQELATTVVNDNKKADTRTINVAVEPGY	
SEQ1	(45)	YYFQTVLNNASFWKEYKFYNANNQELATTVVNDNKKADTRTINVAVEPGY	
		151	200
ADA89581	(151)	KSLTTKVHIVVPQINYNHRYTTHLEFEKA IPTLADAAKPNNVKPVQPKPA	
SEQ1	(95)	KSLTTKVHIVVPQINYNHRYTTHLEFEKA IPTLADAAKPNNVKPVQPKPA	
		201	250
ADA89581	(201)	QPKTPTEQTKPVQPKVEKVKPTVTTT SKVEDNHSTKVVSTD TTKDQ----	
SEQ1	(145)	QPKTPTEQTKPVQPKVEKVKPTVTTT SKVEDNHSTKVVSTD TTKDQTKTQ	
		251	300
ADA89581	(247)	-----	
SEQ1	(195)	TAHTVKTAQTAQEONKVQTPVKDVATAKSESNNQAVSDNKSQQTNKVTKH	
		301	316
ADA89581	(247)	-----	
SEQ1	(245)	NETPKQASKAKELPKT	

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SEQUENCE ALIGNMENT 2

		1		50
SEQ1	(1)	MGTQVSQATSQPINFQVQKDGSSSEKSHMDDYMQHPGKVIKQNNKYYFQTV		
AAU75475	(1)	-----		
		51		100
SEQ1	(51)	LNNASFWKEYKFYNANNQELATTVVNDNKKADTRTINVAVEPGYKSLTTK		
AAU75475	(1)	-----		
		101		150
SEQ1	(101)	VHIVVPQINYNHRYTTHLEFEKAIPTLADAAKPNNVKPVQPKPAQPKTPT		
AAU75475	(1)	-----		
		151		200
SEQ1	(151)	EQTKPVQPKVEKVKPTVTTTTSKVEDNHSTKVSTDTTKDQTKTQTAHTVK		
AAU75475	(1)	-----DQTKTQTAHTVK		
		201		250
SEQ1	(201)	TAQTAQEONKVQTPVKDVATAKSESNNQAVSDNKSQQTNKVTKHNETPKQ		
AAU75475	(13)	TAQTAQEONKVQTPVKDVATAKSESNNQAVSDNKSQQTNKVTKHNETPKQ		
		251		294
SEQ1	(251)	ASKAKELPKT-----		
AAU75475	(63)	ASKAKELPKTGLTSVDNFISTVAFATLALLGSLSLLLFKRKESK		

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SEQUENCE ALIGNMENT 3

		1	50
ADA89548	(1)	MTKHYLNSKYQSEQRSSAMKKITMG TASII LGSLVYIGADSQQVNAATEA	
SEQ1	(1)	-----	
		51	100
ADA89548	(51)	TNATNNQSTQV SQATSQPIN FQVKDGSSEKSHMDDYMQHPGKVIKQNNK	
SEQ1	(1)	-----MGTQV SQATSQPIN FQVKDGSSEKSHMDDYMQHPGKVIKQNNK	
		101	150
ADA89548	(101)	YYFQTVLNNASFWKEYKFYNANNQELATTVVNDNKKADTRTINVAVEPGY	
SEQ1	(45)	YYFQTVLNNASFWKEYKFYNANNQELATTVVNDNKKADTRTINVAVEPGY	
		151	200
ADA89548	(151)	KSLTTKVHIVVPQINYNHRYTTHLEFEKAIPTLADAAKPNNVKPVQPKPA	
SEQ1	(95)	KSLTTKVHIVVPQINYNHRYTTHLEFEKAIPTLADAAKPNNVKPVQPKPA	
		201	250
ADA89548	(201)	QPKTPTEQTKPVQPKVEKVKPTVTTT SKVEDNHSTKVVSTDTTKDQTKTQ	
SEQ1	(145)	QPKTPTEQTKPVQPKVEKVKPTVTTT SKVEDNHSTKVVSTDTTKDQTKTQ	
		251	300
ADA89548	(251)	TAHTVKTAQTAQEONKVQTPVKDVATAKSESNNQAVSDNKSQQTNKVTKH	
SEQ1	(195)	TAHTVKTAQTAQEONKVQTPVKDVATAKSESNNQAVSDNKSQQTNKVTKH	
		301	350
ADA89548	(301)	NETPKQASKAKELPKTGLTSVDNFISTVAFATLALLGSLSLLLFKRKESK	
SEQ1	(245)	NETPKQASKAKELPKT-----	